

## Animal Hepacivirus and World Hepatitis Day

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July 28<sup>th</sup> is celebrated as World Hepatitis Day. The day is to draw attention of people all around the world to support prevention of hepatitis, testing and treatment. Globally, events are organized to showcase best practices, develop collaborations and generate funding. The global hepatitis report, 2017, by world health organization (WHO) reported a collective 1.34 million deaths in 2015 by viral hepatitis. Among them 71 million people were estimated to have chronic hepatitis C infection. Hepatitis C is caused by the infection of hepatitis C virus (HCV) [1-3]. HCV chronically infects 3% of the global population, and more than 70% of people acutely infected with HCV develop chronic viral hepatitis leading to liver cirrhosis and hepatocellular carcinoma.

HCV belong to the genus hepacivirus. Recent efforts from scientists involved with zoonotic viral diseases had expanded the known phylogenetic and host diversity of genus hepacivirus considerably. This genus includes bat hepacivirus (BHV), canine hepacivirus (CHV), GB Hepacivirus (GBV-B), guereza hepacivirus (GHV), non-primate hepacivirus (NPHV), and rodent hepacivirus (RHV). Viral zoonosis accounts for multitude of the emerging human viral diseases [4,5].

Viruses of genus hepacivirus (excluding HCV) had been identified in cattle, dogs, horses, rodents, bats, old world primates, and graceful cat shark [6]. Interestingly the animal hepacivirus RNA or antibodies were absent in cat, deer, donkey, human, pig and rabbit. The infectious virus are spread all over the world and had been identified in animals from Australia, Germany, Brazil, Cameroun, D. R. Congo, France, Gabon, Ghana, Guatemala, Hungary, Japan, Kenya, Mexico, Nigeria, Panama, Papua-New Guinea, South Africa, The Netherlands, Thailand, UK, Uganda, and USA [7].

Overall it suggests that hepacivirus can cross species-barriers in a geographically independent manner. Transmission between different animal species may account for the expanded host range. A better understanding of zoonotic potential of these animal hepaciviruses needs to be studied. Further, since HCV in human has several genotypes, it indicates toward a probability of different HCV genotypes evolving from individual transmission events. A detailed study of evolution of hepacivirus in general and HCV in particular may aid in understanding important determinants of these viruses. With the advent of direct acting antiviral agents against HCV, a cure is available for humans. However, development of a vaccine against HCV is lagging far behind. With this developing knowledge of animal hepacivirus, the scope of hepatitis prevention and treatment should be broadened and animal infection should be taken in to consideration.

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